

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (1) AUCKLAND UNISERVICES LIMITED, a duly incorporated New Zealand company c/- The University of Auckland, 58 Symonds Street, Auckland, New Zealand.
- (2) TITLE OF INVENTION: Developmental Tyrosine Kinases and their Ligands.
- (3) NUMBER OF SEQUENCES: 16
- (4) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: A J PARK & SON
 - (B) STREET: HUDDART PARKER BUILDING, POST OFFICE SQUARE
 - (C) CITY: P O BOX 949, WELLINGTON
 - (D) COUNTRY: NEW ZEALAND
- (5) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5,DS,HD FLOPPY DISC
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATION SYSTEM: MS-DOS
 - (D) SOFTWARE: WORD PERFECT 5.1 FOR DOS
- (6) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 16-FEBRUARY 1994
 - (C) CLASSIFICATION
- (7) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BENNETT, MICHAEL R.
- (8) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: (64 4) 473 8278
 - (B) TELEFAX: (64 4) 472 3358

(2) INFORMATION FOR SEQUENCE ID NO. 1:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 874 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: PROTEIN
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 1:

Met	Gly	Trp	Pro	Gly	Leu	Arg	Pro	Leu	Leu	Leu	Ala	Gly
1				5					10			
Leu	Ala	Ser	Leu	Leu	Leu	Pro	Gly	Ser	Ala	Ala	Ala	Gly
	15					20					25	

Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly
40					45					50		
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr
		55					60					65
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser
				70					75			
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val
	80					85					90	
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys
			95					100				
Asp	Gly	Glu	Gly	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu
105					110					115		
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys
		120				125					130	
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser
			135					140				
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr
	145					150					155	
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro
			160					165				
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg
170					175					180		
Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu
		185				190					195	
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro
				200					205			
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser
	210					215					220	
Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp
			225					230				
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala
235					240					245		
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val
		250					255				260	
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala
				265					270			
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn
	275					280					285	
Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe
			290					295				
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn
300					305					310		
Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu
		315					320				325	
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro
				330					335			
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly
	340					345					350	
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn
			355					360				
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg
365					370					375		
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser
		380					385					390
Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg
				395					400			
Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	Pro	Val
	405					410				415		
Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala
			420					425				
Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	Glu	Thr
430					435					440		
Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly
		445					450					455
Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn
				460					465			

Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser
Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp
Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	Arg	Met
Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln
Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val
Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile
Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe
Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	Ser	Leu
Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	Val
Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe
Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu
Pro	Leu	Gln	Thr	Leu	Val	Arg	Phe	Met	Val	Asp	Ile	Ala
Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	Ile	His
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	Glu	Asp
Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys
Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser
Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala
Asp	Asn	Leu	Tyr	Thr	Val	His	Ser	Asp	Val	Trp	Ala	Phe
Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	Gln	Thr
Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn	Tyr
Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys
Met	Glu	Glu	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser
Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg
Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	His	Leu	Ser	Val	Leu
Ser	Thr	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	Glu	Arg
Ala	Glu	Gln	Pro	Thr	Glu	Ser	Gly	Ser	Pro	Glu	Leu	His
Cys	Gly	Glu	Arg	Ser	Ser	Ser	Glu	Ala	Gly	Asp	Gly	Ser
Gly	Val	Gly	Ala	Val	Gly	Gly	Ile	Pro	Ser	Asp	Ser	Arg
Tyr	Ile	Phe	Ser	Pro	Gly	Gly	Leu	Ser	Glu	Ser	Pro	Gly
Gln	Leu	Glu	Gln	Gln	Pro	Glu	Ser	Pro	Leu	Asn	Glu	Asn
Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His
Ser	Ser	Cys				865					870	

(3) INFORMATION FOR SEQUENCE ID NO. 2:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 850 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 2:

											Ala 1	Gly
Leu	Lys	Leu 5	Met	Gly	Ala	Pro	Val 10	Lys	Met	Thr	Val	Ser 15
Gln	Gly	Gln	Pro	Val 20	Lys	Leu	Asn	Cys	Ser 25	Val	Glu	Gly
Met	Glu 30	Asp	Pro	Asp	Ile	His 35	Trp	Met	Lys	Asp	Gly 40	Thr
Val	Val	Gln	Asn 45	Ala	Ser	Gln	Val	Ser 50	Ile	Ser	Ile	Ser
Glu 55	His	Ser	Trp	Ile	Gly 60	Leu	Leu	Ser	Leu	Lys 65	Ser	Val
Glu	Arg	Ser 70	Asp	Ala	Gly	Leu	Tyr 75	Trp	Cys	Gln	Val	Lys 80
Asp	Gly	Glu	Glu	Thr 85	Lys	Ile	Ser	Gln	Ser 90	Val	Trp	Leu
Thr	Val 95	Glu	Gly	Val	Pro	Phe 100	Phe	Thr	Val	Glu	Pro 105	Lys
Asp	Leu	Ala	Val 110	Pro	Pro	Asn	Ala	Pro 115	Phe	Gln	Leu	Ser
Cys 120	Glu	Ala	Val	Gly	Pro 125	Pro	Glu	Pro	Val	Thr 130	Ile	Tyr
Trp	Trp	Arg 135	Gly	Leu	Thr	Lys	Val 140	Gly	Gly	Pro	Ala	Pro 145
Ser	Pro	Ser	Val	Leu 150	Asn	Val	Thr	Gly	Val 155	Thr	Gln	Arg
Thr	Glu 160	Phe	Ser	Cys	Glu	Ala 165	Arg	Asn	Ile	Lys	Gly 170	Leu
Ala	Thr	Ser	Arg 175	Pro	Ala	Ile	Val	Arg 180	Leu	Gln	Ala	Pro
Pro 185	Ala	Ala	Pro	Phe	Asn 190	Thr	Thr	Val	Thr	Thr 195	Ile	Ser
Ser	Tyr	Asn 200	Ala	Ser	Val	Ala	Trp 205	Val	Pro	Gly	Ala	Asp 210
Gly	Leu	Ala	Leu 215	Leu	His	Ser	Cys	Thr	Val 220	Gln	Val	Ala
His	Ala 225	Pro	Gly	Glu	Trp	Glu 230	Ala	Leu	Ala	Val	Val 235	Val
Pro	Val	Pro	Pro 240	Phe	Thr	Cys	Leu	Leu 245	Arg	Asn	Leu	Ala
Pro 250	Ala	Thr	Asn	Tyr	Ser 255	Leu	Arg	Val	Arg	Cys 260	Ala	Asn
Ala	Leu	Gly 265	Pro	Ser	Pro	Tyr	Gly 270	Asp	Trp	Val	Pro	Phe 275
Gln	Thr	Lys	Gly	Leu 280	Ala	Pro	Ala	Arg	Ala 285	Pro	Gln	Asn
Phe	His 290	Ala	Ile	Arg	Thr	Asp 295	Ser	Gly	Leu	Ile	Leu 300	Glu
Trp	Glu	Glu	Val 305	Ile	Pro	Glu	Asp	Pro 310	Gly	Glu	Gly	Pro
Leu 315	Gly	Pro	Tyr	Lys	Leu 320	Ser	Trp	Val	Gln	Glu 325	Asn	Gly
Thr	Gln	Asp 330	Glu	Leu	Met	Val	Glu 335	Gly	Thr	Arg	Ala	Asn 340
Leu	Thr	Asp	Trp	Asp 345	Pro	Gln	Lys	Asp	Leu 350	Ile	Leu	Arg
Val	Cys 355	Ala	Ser	Asn	Ala	Ile 360	Gly	Asp	Gly	Pro	Trp 365	Ser

Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg
Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	Pro	Val
380					385					390		
Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala
		395					400					405
Leu	Ala	Leu	Ile	Leu	Arg	Arg	Lys	Arg	Arg	Lys	Glu	Thr
				410					415			
Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly
		420				425					430	
Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn
			435					440				
Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser
445					450					455		
Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp
		460					465					470
Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	Arg	Met
				475					480			
Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln
		485				490					495	
Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val
			500					505				
Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile
510					515					520		
Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe
		525				530						535
Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	Ser	Leu
				540					545			
Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	Val
		550				555					560	
Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe
			565					570				
Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu
575					580					585		
Pro	Leu	Gln	Thr	Leu	Val	Arg	Phe	Met	Val	Asp	Ile	Ala
		590					595					600
Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	Ile	His
				605					610			
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	Glu	Asp
	615					620					625	
Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys
			630					635				
Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser
640					645					650		
Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala
		655					660					665
Asp	Asn	Leu	Tyr	Thr	Val	His	Ser	Asp	Val	Trp	Ala	Phe
				670					675			
Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	Gln	Thr
	680					685					690	
Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn	Tyr
			695					700				
Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys
705					710					715		
Met	Glu	Glu	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser
		720					725					730
Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg
				735					740			
Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	His	Leu	Ser	Val	Leu
		745				750					755	
Ser	Thr	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	Glu	Arg
			760					765				
Ala	Glu	Gln	Pro	Thr	Glu	Ser	Gly	Ser	Pro	Glu	Leu	His
770					775					780		
Cys	Gly	Glu	Arg	Ser	Ser	Ser	Glu	Ala	Gly	Asp	Gly	Ser
		785					790					795
Gly	Val	Gly	Ala	Val	Gly	Gly	Ile	Pro	Ser	Asp	Ser	Arg
				800					805			

Tyr	Ile	Phe	Ser	Pro	Gly	Gly	Leu	Ser	Glu	Ser	Pro	Gly
Gln	Leu	Glu	Gln	Gln	Pro	Glu	Ser	Pro	Leu	Asn	Glu	Asn
Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His
835					840					845		
Ser	Ser	Cys										
		850										

(4) INFORMATION FOR SEQUENCE ID NO. 3:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 3:

Met	Gly	Arg	Pro	Gly	Leu	Pro	Pro	Leu	Pro	Leu	Pro	Pro
1				5					10			
Pro	Pro	Arg	Leu	Gly	Leu	Leu	Leu	Ala	Glu	Ser	Ala	Ala
15						20					25	
Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr
			30					35				
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val
40					45					50		
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp
		55					60				65	
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro
				70					75			
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys
		80				85					90	
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln
			95					100				
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val
105					110					115		
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu
		120					125				130	
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln
				135					140			
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr
145						150					155	
Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro
			160					165				
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr
170					175					180		
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys
		185					190				195	
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln
				200					205			
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys
210						215					220	
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly
			225					230				
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln
235					240					245		
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val
		250					255				260	
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp
				265					270			
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys
275						280					285	
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val
			290					295				
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro
300					305					310		

Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile
		315					320					325
Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu
				330					335			
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp
	340					345					350	
Asn	Gly	Thr	Gln	Asp	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg
			355					360				
Ala	Asn	Leu	Thr	Gly	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile
365					370				375			
Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	Gly	Cys	Gly	Pro
	380					385						390
Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	Arg	Ala
				395					400			
Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val
	405					410					415	
Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Val	Thr	Ala
			420					425				
Ala	Ala	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys
430					435					440		
Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala
		445					450					455
Arg	Gly	Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser
				460					465			
Phe	Asn	Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu
	470					475					480	
Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu
			485					490				
Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly
495					500					505		
Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu
		510					515					520
Ala	Gln	Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val
				525					530			
Ala	Val	Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser
535						540					545	
Asp	Ile	Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys
			550					555				
Glu	Phe	Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val
560					565					570		
Ser	Leu	Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro
		575					580					585
Met	Val	Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His
				590					595			
Ala	Phe	Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe
	600					605					610	
Asn	Leu	Pro	Leu	Gln	Thr	Leu	Ile	Arg	Phe	Met	Val	Asp
			615					620				
Ile	Ala	Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe
625					630					635		
Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala
		640					645					650
Glu	Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser
				655					660			
Arg	Lys	Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys
	665					670					675	
Ala	Ser	Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser
			680					685				
Leu	Ala	Asp	Asn	Leu	Tyr	Thr	Val	Gln	Ser	Asp	Val	Trp
690					695					700		
Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly
		705					710					715
Gln	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr
				720					725			
Asn	Tyr	Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro
	730					735					740	
Glu	Cys	Met	Glu	Asp	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys
			745					750				

Trp 755	Ser	Ala	Asp	Pro	Lys 760	Gln	Arg	Pro	Ser	Phe 765	Thr	Cys
Leu	Arg	Met 770	Glu	Leu	Glu	Asn	Ile 775	Leu	Gly	Gln	Leu	Ser 780
Val	Leu	Ser	Ala	Ser 785	Gln	Asp	Pro	Leu	Tyr 790	Ile	Asn	Ile
Glu	Arg 795	Ala	Glu	Glu	Pro	Thr	Val	Gly	Gly	Ser	Leu	Glu
Leu	Pro	Gly	Arg 810	Asp	Gln	Pro	Tyr	Ser 815	Gly	Ala	Gly	Asp
Gly 820	Ser	Gly	Met	Gly	Ala 825	Val	Gly	Gly	Thr	Pro 830	Ser	Asp
Cys	Arg	Tyr 835	Ile	Leu	Thr	Pro	Gly 840	Gly	Leu	Ala	Glu	Gln 845
Pro	Gly	Gln	Ala	Glu 850	His	Gln	Pro	Glu	Ser 855	Pro	Leu	Asn
Glu	Thr 860	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu 870	Leu
Pro	His	Ser	Ser 875	Cys								

(5) INFORMATION FOR SEQUENCE ID NO. 4:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 850 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 4:

Ala 1	Gly	Leu	Lys	Leu 5	Met	Gly	Ala	Pro	Val 10	Lys	Leu	Thr
Val	Ser 15	Gln	Gly	Gln	Pro	Val 20	Lys	Leu	Asn	Cys	Ser 25	Val
Glu	Gly	Met	Glu 30	Glu	Pro	Asp	Ile	Gln 35	Trp	Val	Lys	Asp
Gly 40	Ala	Val	Val	Gln	Asn 45	Leu	Asp	Gln	Leu	Tyr 50	Ile	Pro
Val	Ser	Glu 55	Gln	His	Trp	Ile	Gly 60	Phe	Leu	Ser	Leu	Lys 65
Ser	Val	Glu	Arg	Ser 70	Asp	Ala	Gly	Arg	Tyr 75	Trp	Cys	Gln
Val	Glu 80	Asp	Gly	Gly	Glu	Thr 85	Glu	Ile	Ser	Gln	Pro 90	Val
Trp	Leu	Thr	Val 95	Glu	Gly	Val	Pro	Phe 100	Phe	Thr	Val	Glu
Pro 105	Lys	Asp	Leu	Ala	Val 110	Pro	Pro	Asn	Ala	Pro 115	Phe	Gln
Leu	Ser	Cys 120	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr 130
Ile	Val	Trp	Trp 135	Arg	Gly	Thr	Thr	Lys	Ile 140	Gly	Gly	Pro
Ala	Pro 145	Ser	Pro	Ser	Val	Leu 150	Asn	Val	Thr	Gly	Val 155	Thr
Gln	Ser	Thr	Met 160	Phe	Ser	Cys	Glu	Ala 165	His	Asn	Leu	Lys
Gly 170	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His 180	Leu	Gln
Ala	Leu	Pro 185	Ala	Ala	Pro	Phe	Asn 190	Ile	Thr	Val	Thr	Lys 195
Leu	Ser	Ser	Ser	Asn 200	Ala	Ser	Val	Ala	Trp 205	Met	Pro	Gly
Ala	Asp 210	Gly	Arg	Ala	Leu	Leu 215	Gln	Ser	Cys	Thr	Val 220	Gln
Val	Thr	Gln	Ala 225	Pro	Gly	Gly	Trp	Glu 230	Val	Leu	Ala	Val

Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp
235				240						245		
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys
		250				255						260
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val
				265					270			
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro
	275					280					285	
Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile
			290					295				
Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu
300					305					310		
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp
		315					320					325
Asn	Gly	Thr	Gln	Asp	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg
				330					335			
Ala	Asn	Leu	Thr	Gly	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile
	340					345					350	
Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	Gly	Cys	Gly	Pro
			355					360				
Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	Arg	Ala
365					370					375		
Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val
		380					385					390
Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Val	Thr	Ala
				395					400			
Ala	Ala	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys
	405					410					415	
Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala
			420					425				
Arg	Gly	Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser
430					435					440		
Phe	Asn	Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu
		445					450					455
Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu
				460					465			
Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly
	470					475					480	
Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu
			485					490				
Ala	Gln	Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val
495					500					505		
Ala	Val	Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser
		510					515					520
Asp	Ile	Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys
				525					530			
Glu	Phe	Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val
	535					540					545	
Ser	Leu	Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro
			550					555				
Met	Val	Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His
560					565					570		
Ala	Phe	Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe
		575					580					585
Asn	Leu	Pro	Leu	Gln	Thr	Leu	Ile	Arg	Phe	Met	Val	Asp
				590					595			
Ile	Ala	Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe
	600					605					610	
Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala
			615					620				
Glu	Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gln	Leu	Ser
625					630				635			
Arg	Lys	Ile	Tyr	Ser	Gly	Asp	Tyr	Arg	Gln	Gly	Cys	
		640					645				650	
Ala	Ser	Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser
				655					660			
Leu	Ala	Asp	Asn	Leu	Tyr	Thr	Val	Gln	Ser	Asp	Val	Trp
	665					670					675	

Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly
Gln	Thr	Pro	680	Tyr	Ala	Gly	Ile	685	Ala	Glu	Ile	Tyr
690	Asn	Tyr	Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro
705	Glu	Cys	Met	Asp	Val	Tyr	Asp	710	Leu	Met	Tyr	Gln
720	Trp	Ser	Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr
730	Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	Gln	Leu
745	Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro	Glu	Tyr	Ile	Asn
760	Glu	Arg	Ala	Glu	Glu	Pro	Thr	Val	Gly	Gly	Ser	Leu
770	Leu	Pro	Gly	Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly
785	Gly	Ser	Gly	Met	Gly	Ala	Val	Gly	Gly	Thr	Pro	Ser
795	Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	Gly	Leu	Ala	Glu
810	Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	Leu
825	Glu	Thr	Gln	Arg	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu
835	Pro	His	Ser	Ser	Cys	850						845

(6) INFORMATION FOR SEQUENCE ID NO. 5:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 5:

Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Ala	Gly
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Val	Ser
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg

Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu
Ala	160	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Pro
Pro	175	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Thr	Thr	Ile	Ser
185	200	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala
Ser	215	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val
Gly	225	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val
His	230	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala
Pro	240	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala
250	255	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro
Ala	265	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln
Gln	280	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu
Phe	290	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly
Trp	305	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly
Leu	315	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala
Thr	330	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu
Leu	345	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp
Val	355	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly
Gln	370	Gly	Pro	Pro	His	Ser	Arg					Arg
380												

(7) INFORMATION FOR SEQUENCE ID NO. 6:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 6:

Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr
1				5					10			
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val
15						20					25	
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp
			30					35				
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro
40					45					50		
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys
							60				65	
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln
				70					75			
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val
						85					90	
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu
			95					100				
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln
105					110					115		
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr
							125					130

Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro
				135					140			
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr
	145					150					155	
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys
			160					165				
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln
170					175					180		
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys
		185					190					195
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly
				200					205			
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln
	210					215					220	
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val
			225					230				
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp
235					240					245		
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys
		250					255					260
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val
				265					270			
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro
	275					280					285	
Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile
			290					295				
Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu
300					305					310		
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp
		315					320					325
Asn	Gly	Thr	Gln	Asp	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg
				330					335			
Ala	Asn	Leu	Thr	Gly	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile
	340					345					350	
Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	Gly	Cys	Gly	Pro
			355					360				
Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	Arg	Ala
365					370					375		
Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg				
		380					385					

(8) INFORMATION FOR SEQUENCE ID NO. 7:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3919 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 7:

GGCAGGAGTG	TGGAAGGAGC	GCGGTGGCCC	AGCCGCAGCC	CCGGGGACTC	CTCGCTGCTG	60
ACGGCGGTGG	CCGCGGTCT	AGCGGCGCGC	GGGTCCCGGA	CGCCCCGGCC	GAGCGCCGCC	120
CCCCGCCCCC	CCCCGCGGCC	TCCCGCCCCC	CCTCCGCCAC	CCTCCTCTCA	CGGCTCGCGG	180
GCCGGGCGCC	GCATGGTGCG	GCGTCGCCGC	CGATGCCGCT	GAGGCGGAGC	ATGGGGTGGC	240
CGGGGCTCCG	GCCGCTGCTG	CTGGCGGGAC	TGGTCTCTCT	GCTGTCCCCC	GGGTCTGCGG	300
CCGAGGCGCT	GAAGCTCATG	GGCGCCCCAG	TGAAGATGAC	CGTGTCTCAG	GGGCAGCCAG	360
TGAAGCTCAA	CTGCAGCGTG	GAGGGGATGG	AGGACCTGGA	CATCCACTGG	ATGAAGGATG	420
GCACCGTGGT	CCAGAATGCA	AGCCAGGTGT	CCATCTCCAT	CAGCGAGCAC	AGCTGGATTG	480
GCTTACTCAG	CCTAAAGTCA	GTGGAGCGGT	CTGATGCTGG	CCTGTACTGG	TGCCAGGTGA	540

AGGATGGGGA	GGAACCAAG	ATCTCTCAGT	CAGTATGGCT	CAGTGTGCA	GGTGTGCCAT	600
TCTTCACAGT	GGAACCAAA	GATCTGGCGG	TGCCACCCAA	TGCCCTTTT	CAGCTGTCTT	660
GTGAGGCTGT	GGGTCTCTCA	GAACCCGTAA	CCATTACTGT	GTGGAGAGGA	CTCACTAAAG	720
TTGGGGGACC	TGCTCCCTCT	CCCTCTGTTT	TAAATGTGAC	AGGAGTGACC	CAGCGCACAG	780
AGTTTTCTTG	TGAAGCCCGC	AACATAAAAG	AGCTGGCCAC	TTCGCCACCA	GCCATTGTTC	840
GCCTTCAAGC	ACCGCCTGCA	GCTCCTTTCA	ACACCACAGT	AACAACGATC	TCCAGGTACA	900
ACGCTAGGCT	GGCCTGGGTG	CCAGGTGCTG	ACGGCCTAGC	TCTGCTGCAT	TCCTGTACTG	960
TACAGTGGGC	AGACGCCCCA	GGAGAATGGG	AGGCCCTTGC	TGTTGTGGTT	CCTGTGCCAC	1020
CTTTTACCTG	CCTGCTTCGG	AACTTGGCCC	CTGCCACCAA	CTACAGCCTT	AGGGTGCCT	1080
GTGCCAATGC	CTTGGGCCCT	TCTCCCTACG	CGCACTGGGT	GCCCTTTCAG	ACAAAGGGCC	1140
TAGCGCCAGC	CAGAGCTCCT	CAGAATTTCC	ATGCCATTCC	TACCGACTCA	GGCCTTATCC	1200
TGGAATGGGA	AGAAGTGATT	CCTGAGGACC	CTGGGGAAGG	CCCCCTAGGA	CCTTATAAGC	1260
TGCTCTGGGT	CCAAGAAAA	GGAACCCAGG	ATGAGCTGAT	GGTGAAGGG	ACCAGGGCCA	1320
ATCTGACCGA	CTGGGATCCC	CAGAAGGACC	TGATTTTGCG	TGTTGTGTCC	TCCAATGCAA	1380
TTGGTGATGG	GCCCTGGAGT	CAGCCACTGT	TGGTGTCTTC	TCATGACCAT	GCAGGGAGGC	1440
AGGGCCCTCC	CCACAGCCGC	ACATCCTGGG	TGCTGTGGTT	CTGGGCGTG	CTCACCGCC	1500
TGATCACAGC	TGCTGCCTTG	GCCCTCATCC	TGCTTCGGAA	GAGACGCAAG	GAGACGCGTT	1560
TCGGGCAAGC	CTTTGACAGT	GTCATGGCCC	GAGGGGAGCC	AGCTGTACAC	TTCGGGGCAG	1620
CCCGATCTTT	CAATCGAGAA	AGGCCTGAAC	GCATTGAGGC	CACATTGGAT	AGCCTGGGGA	1680
TCAGCGATGA	ATTGAAGGAA	AAGCTGGAGG	ATGTCTCAT	TCCAGAGCAG	CAGTTCACCC	1740
TCGGTCGGAT	GTTGGGCAAA	GGAGAGTTTG	GATCAGTGCG	GGAAGCCAG	CTAAAGCAGG	1800
AAGATGGCTC	CTTCGTGAAA	GTGGCAGTGA	AGATGCTGAA	AGCTGACATC	ATTGCCCTCA	1860
GCGACATAGA	AGAGTCTCTC	CGGGAAGCAG	CTGTCATGAA	GGAGTTTGAC	CATCCACACG	1920
TGGCCAAAGC	TGTTGGGGTG	AGCCTCCGGA	GCAGGGCTAA	AGGTCTGCTC	CCCATTCCCA	1980
TGGTCATCCT	GCCCTTCATG	AAACATGGAG	ACTTGCACGC	CTTTCTGCTC	GCCTCCCGAA	2040
TCGGGGAGAA	CCCTTTTAA	CTGCCCTGCG	AGACCCTGGT	CCGGTTCATG	GTGGACATTG	2100
CCTGTGGCAT	GGAGTACCTG	AGCTCCCGGA	ACTTCATCCA	CCGAGACCTA	GCAGCTCGGA	2160
ATTGCATGCT	GGCCGAGGAC	ATGACAGTGT	GTGTGGCTGA	TTTGGACTC	TCTCGGAAAA	2220
TCTATAGCGG	GGACTATTAT	CGTCAGGGCT	GTGCCCTCAA	ATTGCCCTGG	AAGTGGCTGG	2280
CCCTGGAGAG	CTTGGCTGAC	AACTTGATA	CTGTACACAG	TGATGTGTGG	GCCTTCCGGG	2340
TGACCATGTG	GGAGATCATG	ACTCGTGGGC	AGACGCCATA	TGCTGGCATT	GAAAATGCTG	2400
AGATTTACAA	CTACCTCATC	GGCGGGAACC	GCTCGAAGCA	GCCTCCGGAG	TGCATGGAGG	2460
AAGTGATATG	TCTCATGTAC	CAGTGTGGA	GCGCCGACCC	CAAGCAGCGC	CCAAGCTTCA	2520
CGTGTCTGCG	AATGGAACCTG	GAGAACATTC	TGGGCCACCT	GTCTGTGCTG	TCCACGACC	2580
AGGACCCCTT	GTACATCAAC	ATTGAGAGAG	CTGAGCAGCC	TACTGAGAGT	GGCAGCCCTG	2640
AGCTGCACTG	TGGAGACCGA	TCCAGCAGCG	AGGCAGGGCA	CGGCAGTGGC	GTGGGGGCGC	2700
TAGGTGGCAT	CCCCAGTGAC	TCTCGGTACA	TCTTCAGCCC	CGGAGGGCTA	TCCGAGTCAC	2760
CAGGGCAGCT	GGAGCAGCAG	CCAGAAAGCC	CCCTCAATGA	GAACCAGAGG	CTGTGTGTGC	2820
TGCAGCAAGG	GCTACTGCCT	CACAGTAGCT	GTTAACCCCTC	AGGCAGAGGA	AAGTTGGGGC	2880
CCCTGGCTCT	GCTGACCATT	GTGCTGCCTG	ACTAGGCCCA	GTCTGATCAC	AGCCACAGGA	2940
GCAAGGTATG	GAGGCTCCTG	TGGTAGCCCT	CCCAAGCTGT	GCTGGCCGCT	GACGGACCA	3000
AATTGCCCAA	TCCCAGTTCT	TCTTGCAGCC	GCTCTGGCCA	GCCTGGCATC	AGTTCAGGCC	3060
TTGGCTTAGA	GGAGGTGAGC	CAGAGCTGGT	TGCCTGAATG	CAGGCAGCTG	GCAGGAGGGG	3120
AGGGTGGCTA	TGTTTCCATG	GGTACCATTG	GTGTGGATGG	CAGTAAGGGA	GGGTAGCAAC	3180
AGCCCTGTGG	GCCCTTACCC	TCTTGGCTGA	CTTGTCTCTA	CTTTAGTGCA	TGCTTGGAGC	3240
GCCTGCGAGC	CTGGAATCTA	GCATGCCCCA	CCACACTTGG	GCCGAAATGC	CAGGTTTGGC	3300

CCTCTTAAGT	CACAAAGAGA	TGTCCATGTA	TGTTCCCTT	TAGGTGATG	ATTAGGAAGG	3360
GATTGGCACA	CTTGGGTCCC	TAAGCCCTAT	GGCAGGAAAT	GGTGGGATAT	TCTCAGGTCT	3420
GAATCCTCAT	CATCTTCCGT	ATTCCCCACC	CTGCAAAGGC	CTGGAAGTGG	CTGTGGGGCT	3480
CTGAGGCATG	CTGAAGGACA	AAAGATTACA	GAGATCCGAC	TTCAAAAGGC	AGGGTCTGAG	3540
TCTGGCAGGT	GGAGAGGTGC	TAAGGGGCTG	GCCCAGGAGT	CAGGCATTTC	AGGACCCCTC	3600
CAAGCTTCTA	CAGTCTGTCT	GAGCATGCTA	CCAAGCCCCC	AGATACCCCA	AAACTAACAG	3660
AGGCAGTTTT	GCTCGAGCCC	AGCCCTCCCA	CATGATGACC	CTTAGGTCTA	CCCTCCTCTC	3720
TAAATGGACA	TCCTCGTTTG	TCCCAAGTCT	CCAGAGAGAC	TACTGATGGC	TGATGTGGGT	3780
AAGAAAAGTT	CCAGGAACCA	GGGCTGGGGT	GGAACCCAGG	CTGGGGTCGA	GGCAGGCTCT	3840
TGGGCAGGCT	CTTGCTGTGA	GGAACATTTC	TAAGCTATTA	AGTTGCTGTT	TCAAAACAAA	3900
TAAAAATTGAA	ACATAAAGA					3919

(9) INFORMATION FOR SEQUENCE ID NO. 8:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2550 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 8:

GCAGGCCTGA	AGCTCATGGG	GCCCCCAGTG	AAGATGACCG	TGTCTCAGGG	GCAGCCAGTG	60
AAGCTCAACT	GCAGCGTGGA	GGGGATGGAG	GACCCGTGACA	TCCACTGGAT	GAAGGATGGC	120
ACCGTGGTCC	AGAATGCAAG	CCAGGTGTCC	ATCTCCATCA	CGGAGCACAG	CTGGATTGGC	180
TTACTACAGC	TAAAGTCAGT	GGAGCGGTCT	GATGCTGGCC	TGTACTGGTG	CCAGGTGAAG	240
GATGGGGAGG	AAACCAAGAT	CTCTCAGTCA	GTATGGCTCA	CTGTGCAAGG	TGTGCCATTG	300
TTACAGTGG	AACCAAAAGA	TCTGGCGGTG	CCACCCAAATG	CCCCTTTTCA	GCTGTCTTGT	360
GAGGCTGTGG	GTCTCTCAGA	ACCCGTAACC	ATTACTGGT	GGAGAGGACT	CACTAAAGTT	420
GGGGAGCCTG	CTCCCTCTCC	CTCTGTTTTA	AATGTGACAG	GAGTGACCCA	GGGCACAGAG	480
TTTTCTTGTG	AAGCCCGCAA	CATAAAAGGC	CTGGCCACTT	CCCGACCAGC	CATTGTTCCG	540
CTTCAAGCAC	CGCCTGCAGC	TCCTTTCAAC	ACCACAGTAA	CAACGATCTC	CAGCTACAAC	600
GCTAGCTGGG	CCTGGGTGCC	AGGTGCTGAC	GGCCTAGTCT	TGCTGCATTC	CTGTACTGTA	660
CAGGTGGCAC	ACGCCCCAGG	AGAATGGGAG	GCCTTGTGCT	TTGTGGTTCC	TGTGCCACCT	720
TTTACCTGCC	TGCTTCGGAA	CTTGGCCCTT	GCCACCAACT	ACAGCCTTAG	GGTGGCGTGT	780
GCCAATGCCT	TGGGCCCTTC	TCCTCATCGG	GACTGGGTGC	CCTTTCAGAC	AAAGGGCCTA	840
GCGCCAGCCA	GAGCTCCTCA	GAATTTCCAT	GCCATTCGTA	CCGACTCAGG	CCTTATCTCTG	900
GAATGGGAAG	AAGTGATTCC	TGAGGACCCCT	GGGGAAGGCC	CCCTAGGACC	TTATAAGCTG	960
TCCTGGGTCC	AAGAAAATGG	AACCCAGGAT	GAGCTGATGG	TGGAAGGGAC	CAGGGCCAAT	1020
CTGACCGACT	GGGATCCCCA	GAAGGACCTG	ATTTTGCCTG	TGTGTGCCTC	CAATGCAATT	1080
GGTGATGGGC	CCTGGAGTCA	GCCACTGGTG	GTGTCTTCTC	ATGACCATTG	AGGGAGGCAG	1140
GGCCCTCCCC	ACAGCCCGAC	ATCCTGGGTG	CCTGTGGTCC	TGGGCGTGCT	CACCGCCCTG	1200
ATCACAGCTG	CTGCCTTGGC	CCTCATCTCT	CTTCGGAAGA	GACGCAAGGA	GACGCGTTTC	1260
GGGCAAGCCT	TTGACAGTGT	CATGGCCCGA	GGGGAGCCAG	CTGTACACTT	CCGGGCAGCC	1320
CGATCTTTCA	ATCGAGAAAG	GCCTGAACGC	ATTGAGGCCA	CATTGGATAG	CCTGGGCATC	1380
AGCGATGAAT	TGAAGGAAAA	GCTGGAGGAT	GTCTCATTC	CAGAGCAGCA	GTTCAACCTC	1440

GGTCGGATGT	TGGGCAAAAG	AGAGTTTGA	TCAGTGCGGG	AAGCCCAGCT	AAAGCAGGAA	1500
GATGGCTCCT	TCGTGAAAGT	GGCAGTGAAG	ATGCTGAAAG	CTGACATCAT	TGCTCTCAAGC	1560
GACATAGAAG	AGTTTCCTCCG	GGAAAGCAGCT	TGCATGAAGG	AGTTTGACCA	TCCACACGTG	1620
GCCAAGCTTG	TGTGGGTGAG	CCTCCGGAGC	AGGGCTAAAG	GTCGTCTCCC	CATTCCCATG	1680
GTCACTCTGC	CCTTCATGAA	ACATGGAGAC	TTGCACGCCT	TTCTGCTCGC	CTCCCCGAATC	1740
GGGGAGAAAC	CTTTTAACTT	GCCCTGCAG	ACCTTGGTCC	GGTTTCATGGT	GGACATTGGC	1800
TGTGGCATGG	AGTACCTGAG	CTCCCAGAAC	TTATCCACC	GAGACCTAGC	AGCTCGGAAT	1860
TGCATGCTGG	CCGAGGACAT	GACAGTGTGT	GTGGCTGATT	TGGACTCTC	TCGGAAAAATC	1920
TATAGCGGGG	ACTATTATCG	TCAGGGCTGT	GCCTCCAAAT	TGCCCCGCAA	GTGGCTGGCC	1980
CTGGAGAGCT	TGGCTGACAA	CTTGTATACT	GTACACAGTG	ATGTGTGGGC	CTTCGGGGTG	2040
ACCATGTGGG	AGATCATGAC	TCGTGGGCAG	ACGCCATATG	CTGGCATTGA	AAATGCTGAG	2100
ATTTACAAC	ACCTCATCGG	CGGGAACCGC	CTGAAGCAGC	CTCCGGAGTG	CATGGAGGAA	2160
GTGTATGATC	TCATGTACCA	GTGCTGGAGC	GCGCACCCCA	AGCAGCGCCC	AAGTTTCACG	2220
TGCTCTGCGAA	TGGAATCGGA	GAACATTCTG	GGCCACCTGT	CTGTGCTGTC	CACCAGCCAG	2280
GACCCCTTGT	ACATCAACAT	TGAGAGAGCT	GAGCAGCCTA	CTGAGAGTGG	GAGCCCTGAG	2340
CTGCACTGTG	GAGAGCGATC	CAGCAGCGAG	GCAGGGGACG	GCAGTGGCGT	GGGGGCAGTA	2400
GGTGGCATCC	CCAGTGACTC	TCGGTACATC	TTCAAGCCCC	GAGGGCTATC	CGAGTCACCA	2460
GGGCAGCTGG	AGCAGCAGCC	AGAAAGCCCC	CTCAATGAGA	ACCAGAGGCT	GTTGTTGCTG	2520
CAGCAAGGGC	TACTGCCTCA	CAGTAGCTGT				2550

(10) INFORMATION FOR SEQUENCE ID NO. 9:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4364 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (2) MOLECULE TYPE: cDNA

- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 9:

CATTAGATCT	TTACATGAAA	GTAAATTTA	TAAGATTCTT	AGAAAGTCAA	AAGATGATAA	60
CTATTCTCTA	GGATACTAAA	AGCACTCACA	TTATAGAAAA	AAAATCAGTT	AACATATACTC	120
CACAAACATT	AAAGGCTCCC	TATAAAAAAA	CATTTTAAAT	AGGCAAGCCA	CAGAAAGGGC	180
AAATATTAAT	AGTTTGCAAT	ACATATGTAT	GAAAAGGAAT	TGAATCTAGA	ATATTTAACA	240
AAGCTTTACA	ACTCAAAAAA	TACAAAGAAA	ATATTTTCTT	TCCAAATGGC	AAATTACTTA	300
AACAGAACCT	TCACAAAAGA	AGATAAGAA	GTTTAATAAA	CATTGTGAAGC	CATAATAATG	360
ACATCATTTAG	CCATGATGGA	AATGCAAAAT	TAAGTACCAC	TTACATCCA	CAAGAAAAAG	420
ATAAAAAATA	AAGGACTGAG	CTCACCAAA	ATTGGTGAGG	ATGTGGTAAT	ACTGAAATTC	480
TGTGACCGTG	CTCCTGAGGG	TATAACATAT	TACAGGATTT	TTTTGAAAAC	TAGTGGTTCC	540
TTATAAACTT	AATGCCCTGG	CAACCTCACA	CCTATTACT	TAAGAATGAA	AGGGCCCCCG	600
CCTCCTCCCT	CCTCGCTCGC	GGCCCGGGCC	CGGCATGGTG	CGGCGTCGCC	GCCGATGGCG	660
CTGAGGCGGA	GCATGGGGCG	GCCGGGGCTC	CGGCCGCTGC	CGCTCCCGCC	GCCACCGCGG	720
CTCGGGCTGC	TGCTGGCGGA	CTCCGCCGCC	CGAGTCTCGA	AGCTCATGGT	AGCCCGGGTG	780
AAGCTGACAT	TGCTCAGGG	CGAGCCGGTG	AAGCTCAACT	CGAGTGTGGA	GGGGATGGAG	840
GAGCTGACA	TCCAGTGGGT	GAAGGATGGG	GCTGTGGTCC	AGAACTTGA	CCAGTTGTAC	900
ATCCAGTCA	GCGAGCAGCA	CTGGATCGGC	TTCTCAGCC	TGAAGTCAGT	GGAGCGCTCT	960

GACGCCGGCC GGTACTGGTG CCAGTGCGAG GATGGGGGTG AAACCGAGAT CTCCCAGCCA 1020
 GTGTGGCTCA CGGTAGAAGG TGTGCCATTT TTCACAGTGG AGCCAAAAGA TCTGGCAGTG 1080
 CCACCCAATG CCCCTTTCCA ACTGTCTTGT GA IGCTGTGG GTCCCCCTGA ACCTGTTACC 1140
 ATTGTCTGGT GGAGAGGAAC TACGAAGATC GGGGGACCCG CTCCCTCTCC ATCTGTTTTA 1200
 AATGTAACAG GGTGTACCCA GAGCACCATG TTTTCTGTG AAGCTCACAA CCTAAAAGGC 1260
 CTGGCCTCTT CTCGCACAGC CACTGTTTAC CTTCAAGCAC TGCTCGACG CCCCTTCAAC 1320
 ATCACCGTGA CAAAGCTTTC CAGCAGCAAC GCTAGTGTGG CCTGGATGCC AGGTGCTGAT 1380
 GGCCGAGCTC TGCTACAGTC CTGTACAGTT CAGTGACAC AGGCCCCGAG AGGCTGGGAA 1440
 TGCTCGCTG TGTGTGCTCC TGTGCCCCCC TTTACCTGCC TGCTCCGGGA CCTGTGTCCT 1500
 GCCACCAACT ACAGCCTCAG GGTGCGCTGT GCCAATGCCT TGGGGCCCTC TCCTATGCT 1560
 GACTGGGTGC CCTTTACAGC CAAGGGTCTA GCCCCAGCCA GCGCTCCCCA AAACCTCCAT 1620
 GCCATCCGCA CAGATTACAG CCTCATCTTG GAGTGGGAAG AAGTGATCCC CGAGGCCCT 1680
 TTGGAAGGCC CCCTGGGACC CTACAAACTG TCCTGGGTTC AAGACAATGG AACCAGGAT 1740
 GAGCTGACAG TGGAGGGGAC CAGGGCCAAT TTGACAGGCT GGGATCCCCA AAAGGACCTG 1800
 ATCGTACGTC TGTGCGTCTC CAATGCAGTT GGCTGTGGAC CCTGGAGTCA GCCACTGGTG 1860
 GTCTCTTCTC ATGACCGTGC AGGCCAGCAG GGCCTCTCTC ACAGCCGCAC ATCTGGGTA 1920
 CCTGTGCTC TGTGTGTGCT AACGGCCCTG GTGACGGCTG CTGCCCTGGC CCTCATCTG 1980
 CTTCAAAGA GACGGAAGA GACGCGGTTT GGGCAAGCCT TTGACAGTGT CATGGCCCCG 2040
 GGAGAGCCAG CCGTTCACCT CCGGGCAGCC CGGTCTTCA ATCGAGAAAG GCCCGAGCCG 2100
 ATCAGGCCA CATTGGACAG CTTGGGCATC AGCGATGAAC TAAAGGAAA ACTGGAGGAT 2160
 GTGCTCATCC CAGAGCAGCA GTTACCCTG GCGCGATGT TGGCAAAGG AGAGTTTGGT 2220
 TCAGTGGGG AGGCCAGCT GAAGCAAGAG GATGGCTCCT TTGTGAAAT GGCTGTGAAG 2280
 ATGCTGAAAG CTGACATCAT TGCTCAAGC GACATTGAAG AGTTCTCTAG GGAAGCAGCT 2340
 TGCAATGAAG AGTTTGACCA TCCACACGTG GCCAAACTG TTGGGGTAAG CCTCCGGAGC 2400
 AGGGCTAAAG GCGGTCTCCC CATCCCAGT GTCATCTTGC CCTTCATGAA GCATGGGGAC 2460
 CTGACGCTC TCCTGCTCGC CTCCCGATT GGGGAGAACC CCTTAACTT ACCCTCCAG 2520
 ACCCTGATCC GGTTCATGGT GGACATTGCC TGCGGCATGG AGTACCTGAG CTCTCGGAAC 2580
 TTATCCACC GAGACCTGGC TGCTCGGAAT TGCACTGTGG CAGAGGACAT GACAGTGTGT 2640
 GTGGCTGACT TCGACTCTC CCGGAAGATC TACAGTGGGG ACTACTATCG TCAAGGCTGT 2700
 GCCTCCAAAC TGCTGTCAA GTGGCTGGCC CTGGAGAGCC TGCCGACAA CCTGTATAT 2760
 GTGCAGAGT ACGTGTGGCC GTTCGGGGTG ACCATGTGGG AGATCATGAC ACGTGGGCAG 2820
 ACGCCATATG CTGGCATCGA AAACGCTGAG ATTACAACCT ACCTCATTTG CGGGAAACCG 2880
 CTGAAACAGC CTCGAGAGTG TATGGAGGAC GTGTATGATC TCATGTACCA GTGCTGGAGT 2940
 GCTGACCCCA AGCAGCGCCC GAGCTTTACT TGCTCGCAA TGGAACCTGA GAACATCTTG 3000
 GGCCAGCTGT CTGTGCTATC TGCCAGCCAG GACCCCTTAT ACATCAACAT CGAGAGAGCT 3060
 GAGGAGCCCA CTGTGGGAGG CAGCCTGGAG CTACCTGGCA GGGATCAGCC CTACAGTGGG 3120
 GCTGGGGATG GCAGTGGCAT GGGGGCAGTG GGTGGCACTC CCAGTGACTG TCGGTACATA 3180
 CTACCCCGCG GAGGGCTGGC TGAGCAGCCA GGGCAGGCAG AGCACCAAGC AGAGAGTCCC 3240
 CTCAATGAGA CACAGAGGCT TTTGCTGCTG CAGCAAGGGC TACTGCCACA CAGTAGCTGT 3300
 TAGCCACAGC GCAGAGGGCA TCGGGGCCAT TTGGCCGGCT CTGGTGGCCA CTGAGCTGGC 3360
 TGACTAAGCC CCGTCTGACC CCAGCCAGCA CAGCAAGGTG TGGAGGCTCC TGTGGTAGTC 3420
 CTCCCAAGCT GTGCTGGGAA GCCCGACTG ACCAAATCAC CCAATCCCAG TTCTTCTTGC 3480
 AACCACCTCT TGGCCAGCCT GGCATCAGTT TAGGCCTTGG CTTGATGAA GTGGGCCAGT 3540
 CCTGGTTGTC TGAACCCAGC CAGCTGGCAG GAGTGGGGTG GTTATGTTTC CATGGTTACC 3600
 ATGGAGTGTG ATGGCAGTGT GGGGAGGGCA GGTCCAGCTC TGTGGGCCCT ACCCTCTGTC 3660
 TGAGTGTCGCC CTGCTGCTTA AGTGATGCA TTGAGCTGCC TCCAGCTGG TGGCCAGCT 3720

ATTACCACAC	TTGGGGTTTA	AATATCCAGG	TGTGCCCCCTC	CAAGTCAGAA	AGAGATGTCC	3780
TTGTAATATT	CCCTTTTAGG	TGAGGGTTGG	TAAGGGGTTG	GTATCTCAGG	TCTGAATCCTT	3840
CACCATCTTT	CTGATTCCGC	ACCTGCGCTA	CGCCAGGAGA	AGTTGAGGGG	AGCATGCTTC	3900
CCTGCAGCTG	ACCGGGTCAC	ACAAAGGCAT	GCTGGAGTAC	CCAGCCTATC	AGGTGCCCTC	3960
CTTCCAAAGG	CAGCGTGCCG	AGCCAGCAAG	AGGAAGGGGT	GCTGTGAGGC	TTGCCCAGGA	4020
GCAAGTGAGG	CCGGAGAGGA	GTTCCAGAAC	CCTTCTCCAT	ACCCACAATC	TGAGCACGCT	4080
ACCAATATCTC	AAAATATCCT	AAGACTAACA	AAGGCAGCTG	TGTCTGAGCC	CAACCTTCT	4140
AAACGGTGAC	CTTTAGTGCC	AACCTCCCTC	CTAACTGGAC	AGCCTCTTCT	GTCCCAAGTC	4200
TCCAGAGAGA	AATCAGGCT	GATGAGGGGG	AATTCTGGA	ACCTGGACCC	CAGCCTTGGT	4260
GGGGAGGCT	CTGGAATGCA	TGGGGCGGGT	CCTAGCTGTT	AGGGACATTT	CCAAGCTGTT	4320
AGTGCTGT	TAAATAGAA	ATAAATTGA	AGACTAAAG	CCTA		4364

(11) INFORMATION FOR SEQUENCE ID NO. 10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2550 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 10:

GCAGGTCTGA	AGCTCATGGG	AGCCCCGGTG	AAGCTGACAG	TGTCTCAGGG	GCAGCCGGTG	60
AAGCTCAACT	GCAGTGTGGA	GGGGATGGAG	GAGCCTGACA	TCCAGTGGGT	GAAGGATGGG	120
GCTGTGGTCC	AGAAGTTGGA	CCAGTTGTAC	ATCCAGTCA	GCGAGCAGCA	CTGGATCGGC	180
TTCCTCAGCC	TGAAGTCAGT	GGAGCGCTCT	GACGCCGGCC	GGTACTGGTG	CCAGGTGGAG	240
GATGGGGGTG	AAACCGAGAT	CTCCAGCCCA	GTGTGGCTCA	CGGTAGAAGG	TGTGCCATTT	300
TTCACAGTGG	AGCCAAAGAA	TCTGGCAGTG	CCACCCAATG	CCCTTTTCCA	ACTGTCTTGT	360
GAGGCTGTGG	GTCCCCCTGA	ACCTGTTACC	ATTGTCTGGT	GGAGAGGAAC	TACGAAGATC	420
GGGGGACCCG	CTCCCTCTCC	ATCTGTTTTA	AATGTAAACG	GGGTGACCCA	GAGCAACATG	480
TTTTCCTGTG	AAGCTCACAA	CCTAAAAGGC	TGGGCTCTTT	CTCGCACAGC	CAGTGTTCAC	540
CTTCAAGCAC	TGCTCGCAGC	CCCTTCAAC	ATCACCGTGA	CAAAGCTTTC	CAGCAGCAAC	600
GCTAGTGTGG	CCTGGATGCC	AGGTGCTGAT	GGCCGAGCTC	TGCTACAGTC	CTGTACAGTT	660
CAGGTGACAC	AGGCCCCAGG	AGGCTGGGAA	GTCCCTGGCTG	TTGTGGTCCC	TGTGCCCCCC	720
TTTACCTGCC	TGCTCCGGGA	CCTGGTGCCT	GCCACCAACT	ACAGCCTCAG	GGTGCCTGT	780
GCCAATGCCT	TGGGGCCCTC	TCCCTATGCT	GACTGGGTGC	CCTTTCAGAC	CAAGGGTCTA	840
GCCCCAGCCA	GCCTCCCCCA	AAACTTCCAT	GCCATCCGCA	CAGATTACAG	CCTCATCTTG	900
GAGTGGGAAG	AAGTGATCCC	CGAGGCCCTC	TTGGAAGGCC	CCCTGGGACC	CTCAAAACTG	960
TCCTGGGTTT	AAGACAAATG	AAACCAGGAT	GAGCTGACAG	TGGAGGGGAC	CAGGGCCAAT	1020
TTGACAGGCT	GGGATCCCCA	AAAGGACCTG	ATCGTACGTG	TGTGCGTCTC	CAATGCAAGT	1080
GGCTGTGGAC	CCTGGAGTCA	GCCACTGGTG	GTCTCTTCTC	ATGACCGTGC	AGGCCAGCAG	1140
GGCCCTCCTC	ACAGCCGCAC	ATCCTGGGTA	CCTGTGGTCC	TTGGTGTGCT	AACGGCCCTG	1200
GTGACGGCTG	CTGCCCTGGC	CCTCATCTCT	CTTCGAAAGA	GACGGAAGA	GACGCGGTTT	1260
GGGCAAGCTG	TTGACAGTGT	CATGGCCCGG	GGAGAGCCAG	CCGTTCACCT	CCGGGACGCT	1320
CGGTCTCTCA	ATCGAGAAAG	GCCCGAGCGC	ATCGAGGCCA	CATTGGGACG	CTTGGGACAT	1380
AGCGATGAAC	TAAAGGAAAA	ACTGGAGGAT	GTGCTCATCC	CAGAGCAGCA	GTTACACCTG	1440

GGCCGGATGT	TGGGCAAAGG	AGAGTTTGGT	TCAGTGGCGG	AGGCCAGCT	GAAGCAAGAG	1500
GATGGCTCCT	TTGTGAAAGT	GGCTGTGAAG	ATGCTGAAAG	CTGACATCAT	TGCTCAAGC	1560
GACATTGAAG	AGTTCCCTAG	GGAAGCAGCT	TGCATGAAGG	AGTTTGACCA	TCCACACGTG	1620
GCCAAACTTG	TTGGGGTAAG	CCTCCGGAGC	AGGGCTAAAG	GCCGTCTCCC	CATCCCCATG	1680
GTCACTTTGC	CCTTCAATGAA	GCATGGGGAC	CTGCATGCCT	TCCTGCTCGC	CTCCCGGATT	1740
GGGGAGAACC	CCTTTAACTT	ACCCCTCCAG	ACCCTGATCC	GGTTCATGGT	GGACATTGCC	1800
TGCGGCATGG	AGTACCTGAG	CTCTCGGAAC	TTCATCCACC	GAGACCTGGC	TGCTCGGAAT	1860
TGCACTGTGG	CAGAGGACAT	GACAGTGTGT	GTGGCTGACT	TCGGACTCTC	CCGGAAGATC	1920
TACAGTGGGG	ACTACTATCG	TCAAGGCTGT	GCCTCCAAAC	TGCTGTCAA	GTGGCTGGCC	1980
CTGGAGAGCC	TGGCCGACAA	CCTGTATACT	GTGCAGAGTG	ACGTGTGGGC	GTTCCGGGGT	2040
ACCATGTGGG	AGATCATGAC	ACGTGGGCAG	ACGCCATATG	CTGGCATCGA	AAACCGTGAG	2100
ATTTACAAC	ACCTCATTGG	CGGGAACCGC	CTGAACAGC	CTCCGGAGTG	TATGGAGGAC	2160
GTGTATGATC	TCATATACCA	GTGCTGGAGT	GTGACCCCA	AGCAGCGCCC	GAGCTTTACT	2220
TGTCGTGGAA	TGGAACCTGA	GAAATCTTTG	GGCCAGCTGT	CTGTGCTATC	TGCCAGCCAG	2280
GACCCCTTAT	ACATCAACAT	CGAGAGAGCT	GAGGAGCCCA	CTGTGGGAGG	CAGCCTGGAG	2340
CTACCTGGCA	GGGATCAGCC	CTACAGTGGG	GCTGGGGATG	GCACTGGCAT	GGGGGACAGT	2400
GGTGGCACTC	CCAGTGACTG	TGGGTACATA	CTCACCCCGG	GAGGGCTGGC	TGAGCAGCCA	2460
GGGCAGGCAG	AGCACCAGCC	AGAGAGTCCC	CTCAATGAGA	CACAGAGGCT	TTTGTCTGTG	2520
CAGCAAGGGC	TACTGCCACA	CAGTAGCTGT				2550

(12) INFORMATION FOR SEQUENCE ID NO. 11:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1158 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 11:

GCAGGCGCTGA	AGCTCATGGG	CGCCCCAGTG	AAGATGACCG	TGTCTCAGGG	GCAGCCAGTG	60
AAGCTCAACT	GCAGCGTGGA	GGGGATGGAG	GACCTGACA	TCCACTGGAT	GAAGGATGGC	120
ACCGTGGTCC	AGAATGCAAG	CCAGGTGTCC	ATCTCCATCA	GCGAGCACAG	CTGGATTGGC	180
TTACTCAGCC	TAAAGTCAGT	GGAGCGGTCT	GATGCTGGCC	TGTACTGGTG	CCAGGTGAAG	240
GATGGGGAGG	AAACCAAGAT	CTCTCAGTCA	GTATGGGTCA	CTGTCCGAAG	TGTGCCATTG	300
TTACAGATGG	AACCAAAAGA	TCTGGCGGTG	CCACCAATG	CCCTTTTCA	GCTGTCTTGT	360
GAGGCTGTGG	GTCTTCCAGA	ACCCGTAACC	ATTACTGGT	GGAGAGGACT	CACATAAGTT	420
GGGGGACCTG	CTCCCTCTCC	CTCTGTTTTA	AATGTGACAG	GAGTGACCCA	GCGCACAGAG	480
TTTTCTTGTG	AAGCCCGCAA	CATAAAAGGC	CTGGCCACTT	CCCAGCCAGC	CATTGTTGCG	540
CTTCAAGCAC	CGCCTGCAGC	TCTTTTCAAC	ACCACAGTAA	CAACGATCTC	CAGCTACAAC	600
GCTACGCGTG	CTGCGGTGCC	AGGTGCTGAC	GGCCTAGCTC	TGCTGCATTC	CTGTACTGTA	660
CAGGTGGCAC	ACGCCCCAGG	AGAATGGGAG	GCCCTTGTCT	TTGTGGTTCC	TGTGCCACCT	720
TTTACTCTGCC	TGCTTCGGAA	CTTGGCCCTT	GCCACCAACT	ACAGCCTTAG	GGTGGCGTGT	780
GCCAATGCCT	TGGGCCCTTA	TCCCTACGGC	GACTGGGTGC	CCTTTAGAG	AAAGGCGCTA	840
GCGCCAGCCA	GAGCTTCTCA	GAATTTCCAT	GCCATTGCTA	CCGACTCAGG	CCTTATCCTG	900
GAATGGGAAG	AGTGATTCC	TGAGGACCCT	GGGGAAGGCC	CCCTAGGACC	TTATAAGCTG	960

TCCTGGGTCC	AAGAAATGG	AACCCAGGAT	GAGCTGATGG	TGGAAGGGAC	CAGGGCCAAT	1020
CTGACCGACT	GGGATCCCCA	GAAGGACCTG	ATTTTGCCTG	TGTGTGCCTC	CAATGCAATT	1080
GGTGATGGGC	CCTGGAGTCA	GCCACTGGTG	GTGTCTTCTC	ATGACCATGC	AGGGAGGCAG	1140
GGCCCTCCCC	ACAGCCGC					1158

(13) INFORMATION FOR SEQUENCE ID NO. 12:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1158 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 12:

GCAGGCTCTGA	AGCTCATGGG	AGCCCCGGTG	AAGCTGACAG	TGTCTCAGGG	GCAGCCGGTG	60
AAGCTCAACT	GCAGTGTGGA	GGGGATGGAG	GAGCCTGACA	TCCAGTGGGT	GAAGGATGGG	120
GCTGTGGTCC	AGAACTTGGG	CCAGTTGTAC	ATCCCAGTCA	GCGAGCAGCA	CTGGATCGGC	180
TTCTTCAGCC	TGAAGTCAGT	GGAGCGCTCT	GACGCCGGCC	GGTACTGGTG	CCAGGTGGAG	240
GATGGGGGTG	AAACCGAGAT	CTCCAGCCA	GTGTGGCTCA	CGGTAGAAGG	TGTGCCATT	300
TTACAGTGG	AGCCAAAAGA	TCTGGCAGTG	CCACCCAATG	CCCCTTTCCA	ACTGTCTTGT	360
GAGGCTGTGG	GTCCCCCTGA	ACCTGTTACC	ATTGTCTGGT	GGAGAGGAAC	TACGAAGATC	420
GGGGGACCCG	CTCCCTCTCC	ATCTGTTTAA	AATGTAACAG	GGGTGACCCA	GAGCACCATG	480
TTTTCTCTGT	AAGCTCACAA	CCTAAAAGGC	CTGGCCTCTT	CTCGCACAGC	CACTGTTTAC	540
CTTCAAGCAC	TGCTCGAGC	CCCTTCAAC	ATCACCGTGA	CAAAGCTTTC	CAGCAGCAAC	600
GCTAGTGTGG	CCTGGATGCC	AGGTGCTGAT	GGCCGAGCTC	TGCTACAGTC	CTGTACAGTT	660
CAGGTGACAC	AGGCCCCAGG	AGGCTGGGAA	GTCCCTGGTG	TTGTGGTCCC	TGTGCCCCCC	720
TTTACCTGCC	TGCTCCGGGA	CCTGGTGCCT	GCCACCAACT	ACAGCCTCAG	GGTGCCTGCT	780
GCCAAATGCC	TGGGGCCCTC	TCCCTATGCT	GACTGGGTGC	CCTTTCAGAC	CAAGGGTCTA	840
GCCCCAGCCA	CGCCTCCCCA	AAACCTCCAT	GCCATCCGCA	CAGATTCAGG	CCTCATCTTG	900
GAGTGGGAAG	AAGTGATCCC	CGAGGCCCTT	TGGAAGGCC	CCCTGGGACC	CTACAAACTG	960
TCCTGGGTTC	AAGACAATGG	AACCCAGGAT	GAGCTGACAG	TGGAGGGGAC	CAGGGCCAAT	1020
TTGACAGGCT	GGGATCCCCA	AAAGGACCTG	ATCTACCTGT	TGTGCCTCTC	CAATGCAGTT	1080
GGCTGTGGAC	CCTGGAGTCA	GCCACTGGTG	GTCTCTTCTC	ATGACCGTGC	AGGCCAGCAG	1140
GGCCCTCTCT	ACAGCCGC					1158

(14) INFORMATION FOR SEQUENCE ID NO. 13:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 13:

TGGATGGCAG TAAGGGAGG

(15) INFORMATION FOR SEQUENCE ID NO. 14:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 14:

CTTAAGAGGG GCAAACCTGG

20

(16) INFORMATION FOR SEQUENCE ID NO. 15:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 15:

GCTTAGAGGA GGTGAGCCAG A

21

(17) INFORMATION FOR SEQUENCE ID NO. 16:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 16:

TGGGCAGTGC TGAGTTCC

18